

UNITED STATES DISTRICT COURT  
EASTERN DISTRICT OF NEW YORK

-----X

UNITED STATES OF AMERICA

14-CR-414 (BMC)

-against-

RASHAWN JERMAINE SMALLS

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**MEMORANDUM OF LAW IN SUPPORT OF MOTION TO EXCLUDE EVIDENCE**  
**GENERATED BY USE OF THE FORENSIC STATISTICAL TOOL**  
**AND REQUEST FOR A DAUBERT HEARING**

Deborah A. Colson, Esq.  
Kristen M. Santillo, Esq.  
Colson & Harris LLP  
80 Broad Street  
New York, N.Y. 10004  
(212) 257-6455

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Defendant Rashawn Jermaine Smalls respectfully submits this memorandum of law with the attached Affirmation of Deborah Colson, the Declaration of Dr. Ranajit Chakraborty, and their accompanying exhibits in support of his motion pursuant to Federal Rules of Evidence 702 and 403 to exclude evidence at trial generated by use of the Forensic Statistical Tool (“FST”), and to request a *Daubert* hearing. *See Daubert v. Merrell Dow Pharmaceuticals, Inc.*, 509 U.S. 579, 589 (1993).

## I.

### **PRELIMINARY STATEMENT**

This is a tenuous felon-in-possession case. Mr. Smalls was not arrested until nine months after the incident. Video surveillance from the night of the offense is unclear. And the only purported eyewitness told two different stories to the police. To bolster its case, the government has indicated that it intends to introduce DNA test results generated by a controversial software program known as the Forensic Statistical Tool (“FST”). The FST is unreliable, both independently and as applied to the facts of this case, and its probative value is far outweighed by the prejudice that would result if admitted at trial. The Court should exclude the introduction of DNA evidence here.

The FST is a proprietary software program developed by the New York City Office of the Chief Medical Examiner (“OCME”). The program assigns a statistical weight, called a likelihood ratio (“LR”), to DNA mixtures that cannot be “deconvoluted” or separated into individual profiles. A LR reports a statistical association between the DNA evidence and an individual suspect. There are other LR programs, both online and in development. But the FST’s methodology is unique in that it utilizes a system of fixed parameters, tied to DNA

quantity, for calculating the LR in all cases. Other programs permit customization of the parameters to the specific evidence in a case.

Here, OCME used the FST to compare Mr. Smalls' DNA profile with a DNA mixture extracted from the grip area of the gun he allegedly possessed. OCME concluded that (1) the mixture contained the DNA of at least three people, (2) it "is approximately 4,190 times more probable if the sample originated from Jermaine Smalls and two unknown, unrelated persons than if it originated from three unknown, unrelated persons," and (3) the LR of 4,190 provides "very strong support" that Jermaine Smalls and two unknown, unrelated persons contributed to the mixture.

The Court's role at the intersection of science and the law is to ensure that the criminal justice system operates fairly. When dealing with scientific evidence, a judge must determine whether the evidence is sufficiently relevant and reliable to be heard by a jury. OCME's own validation studies for the FST, the scientific literature, Dr. Chakraborty's expert declaration, and the prior testimony of esteemed scientific experts all demonstrate that the FST is unreliable and not ready for use in court.

There are several core problems with the FST. Most critically, the FST's unique system of fixed parameters fails to account for the specific features of real world crime-scene samples and can have the effect of making the LR higher, thereby prejudicing the defense. Moreover, OCME did not properly apply its own protocols in the testing and interpretation of the samples in this case, and the results of its tests are misleading and prejudicial to Mr. Smalls. By definition, the FST is not generally accepted in the scientific community as OCME is the *only* laboratory in the world to use it. Nor has it been subjected to adequate peer review. The source code has not been published, the program itself is not available for public use or inspection, and much of the

key data used to develop the FST has not been preserved and/or made available for inspection by the scientific community. Cumulatively, these flaws render the FST unreliable under *Daubert*.

To our knowledge, FST evidence has never been used in a federal criminal trial over a defendant's *Daubert* objection. New York State courts are split. In October 2013, a Supreme Court judge in New York County admitted FST evidence in a criminal case following an evidentiary hearing. *People v. Rodriguez*, Sup Ct, NY County, Oct. 24, 2013, Caruthers J., Ind. No. 5471-2009.<sup>1</sup> In November 2014, however, a second Supreme Court judge in Kings County excluded the introduction of FST evidence in the combined cases of *People v. Peaks & Collins*, Sup Ct, Kings County, Nov. 7, 2014, Dwyer, J., Ind. Nos. 80077-2010, 7690-2010. *See* Ex. F to Colson Aff. The Court found that there has been no "general agreement in the scientific community as to the challenged scientific principles." *Id.* at 6.

In exercising its gatekeeper function, the Court should grant our request for a *Daubert* hearing and exclude the FST evidence because (1) OCME's methodology is unreliable under *Daubert*, (2) OCME did not properly apply its own protocols to the testing and interpretation of the evidence in this case, and (3) the admission at trial of any evidence produced by this unreliable methodology would confuse and mislead the jury and cause unfair prejudice to Mr. Smalls.

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<sup>1</sup> Some New York courts have also admitted FST evidence without holding a *Frye* hearing. *See, e.g., People v. Garcia*, 39 Misc.3d 482 (Sup Ct, Bronx County 2013); *People v. Styles*, 40 Misc.3d 1205(A), 2013 N.Y. Slip Op. 51019(U), \*2-3 (Sup Ct, NY County 2013) (citing cases). These decisions are of limited force, however, because the defense was not permitted to introduce expert testimony to counter the prosecution's claims.

## II.

### **FACTUAL BACKGROUND**

#### A.

##### **The Alleged Offense**

On October 19, 2013, at 1:30 a.m., police responded to a report of gunshots being fired near 30-42 Falcon Avenue in Queens, New York. *See* Ex. A to Colson Aff. ¶ 2. Upon arrival at the scene, an officer found Mr. Smalls lying on the corner of Beach 32 Street and Seagirt Boulevard. *Id.* He had been shot multiple times and was subsequently treated at Jamaica Hospital. *Id.* at ¶ 4(a).

Later that night, officers recovered a .25 caliber Raven Arms model MP-25 semi-automatic pistol containing four live rounds from the passenger tire of a blue Town and Country minivan, which was parked at 314 Beach 32 Street. *See* Ex. A to Colson Aff. ¶ 3.

Mr. Smalls was arrested on July 7, 2014, on a criminal complaint charging him with being a felon in possession of a weapon in violation of 18 U.S.C. § 922(g). *Id.* He was indicted on July 24, 2014. *See* Ex. B to Colson Aff.

According to the Complaint, an eyewitness told agents that she and Mr. Smalls had encountered a third party as they were leaving a party on October 19, 2013, and a verbal altercation ensued. *See* Ex. A to Colson Aff. ¶ 4(a). The defense has since learned that the witness' name is Megan Woods. The Complaint further states that Ms. Woods told agents that Mr. Smalls pulled out a silver pistol and fired one shot in the direction of the third party. *Id.* Thereafter, another individual shot at Mr. Smalls approximately five or six times, and Mr. Smalls fell to the ground and could not get up. *Id.* Mr. Smalls then "asked the Witness [Megan Woods] to hide his gun, which the Witness agreed to do. The Witness picked up the silver pistol on the

ground near the defendant and placed it on a tire of a parked vehicle.” *Id.* at ¶ 4(b). Ms. Woods has not yet testified or been subjected to cross-examination to determine the veracity of her statements. Notably, however, she “initially failed to mention that the defendant had fired a shot and that the Witness [she] had hidden the firearm.” *Id.* at ¶ 4, n.2.

On discovery, the government provided a security camera video taken on the night of the incident and a phone call between Mr. Smalls and Ms. Woods, recorded on June 26, 2014, while Mr. Smalls was detained on Riker’s Island. *See* Colson Aff. ¶ 5-6. The video is taken from a distance, with scaffolding obscuring the picture. It is dark. There is no audio. And it is difficult to tell what is transpiring. *Id.* at ¶5. The recorded call is also of limited value. The conversation is largely one-sided. Ms. Woods mentions the gun several times, but Mr. Smalls does not admit possession. He simply responds with one-word answers and asks questions about what evidence the police purportedly have against him. *Id.* at ¶6.

## **B.**

### **The Forensic Evidence and Analysis**

To strengthen its case, the government also intends to introduce forensic evidence allegedly connecting Mr. Smalls to the gun. Mr. Smalls’ fingerprints were not recovered from the gun. NYPD did, however, take three DNA swabs from the gun for testing, which were sent to OCME for comparison with court-ordered DNA swabs taken from Mr. Smalls and Megan Woods. OCME analyzed the DNA evidence from the grip area of the gun with traditional PCR/STR testing and with the FST.

#### **1. Traditional PCR/STR DNA Analysis**

DNA (deoxyribonucleic acid) is the hereditary material found inside all of us that makes us human. *See* Declaration of Dr. Ranajit Chakraborty (“Chakraborty Decl.”) ¶ 12. It is frequently referred to as our “genetic blueprint.” *Id.* DNA is located in every nucleated cell in

the body. *Id.* No two individuals, with the exception of identical twins, will have the same genetic code. *Id.*

A chromosome is the tightly packaged structure of DNA. *Id.* at ¶ 13. Each nucleated human cell contains 22 pairs of chromosomes; one chromosome from each pair is inherited from the individual's father, and the other comes from the individual's mother. *Id.* There is also a 23<sup>rd</sup> pair, which is called the sex. chromosome, X and Y. *Id.*

Most modern forensic analyses look at Short Tandem Repeats ("STRs"), which are small segments of DNA that are repeated in tandem. *See id.* at ¶ 14. STRs are distributed among each person's DNA at specific locations ("loci"). *Id.* An allele is a number that describes the size of the DNA fragment, or the number of repeats of the STR motif, at a location ("locus"). Each individual has two alleles at each locus—one inherited from the mother and one from the father. *Id.* at ¶ 15. If the two alleles at a locus are different, they are known as "heterozygous." *Id.* If they are the same, then they are "homozygous." *Id.*

Generally, 13 core loci are examined, with some laboratories testing two additional loci. *Id.* at ¶ 16. One number is reported for each allele at a locus. *Id.* For example, if one chromosome has 13 repeats of the STR motif and the other has 18 repeats, the result is reported as 13, 18 for the particular locus. *Id.* An individual DNA profile is thus a string of numbers representing the alleles at each of the 13 to 15 loci examined. *Id.* Although many individuals will share a particular allele at a particular locus, the chance that two people will have the same set of alleles at multiple loci decreases as the number of loci examined increases. *Id.* Thus, an analyst can use the observed allele combinations at multiple loci to distinguish one individual from another. *Id.*

Basic forensic DNA analysis involves several steps. First, DNA is extracted from the evidence, the gun in this case. *Id.* at ¶17; *see also* National Institute for Justice, “DNA for the Defense Bar” (June 2012), at 12, *available at* <https://www.ncjrs.gov/pdffiles1/nij/237975.pdf>. In the second step, quantification, the analyst measures the amount of DNA present in the sample. Chakraborty Decl. ¶ 17. The third step is amplification, in which a process called polymerase chain reaction (“PCR”) is applied to the DNA sample. *Id.* PCR makes millions of copies of a particular segment of DNA so that it can be detected and analyzed. *Id.* In the fourth step, a process known as electrophoresis separates the STR fragments by size. *See id.* The data from the electrophoresis then becomes the input for a software program—in this case Genemapper—that converts the data to graphs, which can be formed and presented in a number of ways. *Id.* The labeling and graphs produced by the Genemapper program are called electropherograms. *Id.* Electropherograms contain differing peak heights at the different allelic positions. Once an electropherogram is generated, the analyst reviews it, draws conclusions about the DNA sample, and creates a DNA profile. *Id.* at ¶18. In the final step, the analyst compares the profile created with the suspect’s DNA profile. *Id.*

## 2. DNA Mixtures

A DNA mixture is a sample containing the DNA of two or more individual contributors. Chakraborty Decl. ¶ 19. DNA mixtures cannot be easily “deconvoluted” or separated into individual profiles. *Id.* at ¶ 20. In addition, while the quantification step described above provides an estimate as to the total amount of DNA in a mixture, the quantity of DNA from each individual contributor remains unknown, irrespective of the accuracy of the quantification process. *Id.* at ¶ 21.

### 3. Drop-Out and Drop-In

The process of PCR can result in random errors or “stochastic effects.” *See* Chakraborty Decl. ¶ 24. Two of the most common errors are allele drop-out and allele drop-in. *Id.* Allele drop-out occurs when alleles from the principal donors to a DNA mixture fail to appear in the profile. *Id.* Allele drop-in occurs when alleles not originating from the principal donors to a mixture show up in a DNA profile. *Id.*

Drop-out can also result from degradation. *Id.* at ¶ 25. Dirt, bacteria, and sunlight can all cause DNA degradation. *Id.* Touched DNA is also frequently degraded. *Id.* DNA varies by length, and longer pieces of DNA will break down faster than shorter pieces. That means, when DNA is degraded, some longer pieces of DNA may not be detected. *Id.*

A third reason for drop-out involves the relative proportions of DNA in a DNA mixture. *Id.* at ¶ 26. If the amount of DNA from each contributor is not even, more pieces of one donor’s DNA might be grabbed during sampling and/or electrophoresis, and therefore some alleles will not be detected. *Id.*

As discussed more fully below, the accurate calculations of allele drop-out and drop-in are critical to the successful operation of any LR program, including the FST.

### 4. The FST

The FST is a proprietary software program developed by the OCME. The program examines the alleles found in DNA mixtures that cannot be deconvoluted. Then it determines a statistical weight, or likelihood ratio (“LR”), that the suspect’s DNA is included in the mixture. According to the OCME, the “LR value provides a statistical measurement of the strength of support for one scenario over another, i.e., one scenario being that a known person contributed to a mixture versus the scenario that an unknown, unrelated person contributed instead.” Ex. J to

Colson Aff., NYC Office of Chief Medical Examiner, *Forensic Biology Protocols for Forensic STR Analysis* at 440, available at

<http://www.nyc.gov/html/ocme/downloads/pdf/Fbio/Protocols%20for%20Forensic%20STR%20Analysis.pdf> (hereafter “OCME Forensic STR Analysis Protocol.”) The numerator of the LR includes the data favoring the prosecution scenario, while the denominator includes the data favoring the defense scenario. Chakraborty Decl. ¶ 27.

The FST’s methodology is unique in that it utilizes pre-determined allele drop-out and drop-in rates based on DNA quantity to determine the LR. *Id.* at ¶ 29. *See also* Ex. K to Colson Aff., Adele A. Mitchell *et al.*, *Validation of a DNA mixture statistics tool incorporating allelic drop-out and drop-in*, *Forensic Sci. Int’l: Genetics* 6 749-761, 756 (2012) (hereafter “*FST Validation Study*”) (“The drop-out rate estimates employed by FST depend on DNA template quantity.”) This methodology is discussed in detail in Section IV below. OCME is the only laboratory in the world to calculate the drop-out rate based on DNA quantity.

In addition to calculating the LR, the OCME also offers an interpretation of the strength or weakness of its calculation. OCME’s qualitative interpretations report LR values in accordance with the following table:

<b>Reported Value</b>	<b>Qualitative Interpretation</b>
Less than 0.001	Very strong support for Defense Hypothesis over Prosecution Hypothesis
0.001 to 0.01	Strong support for Defense Hypothesis over Prosecution Hypothesis
0.01 to 0.1	Moderate support for Defense Hypothesis over Prosecution Hypothesis
0.1 to 1	Limited support for Defense Hypothesis over Prosecution Hypothesis
1	No conclusions
1 to 10	Limited Support for Prosecution Hypothesis over Defense Hypothesis
10 to 100	Moderate Support for Prosecution Hypothesis over Defense Hypothesis
100 to 1000	Strong Support for Prosecution Hypothesis over Defense Hypothesis
Greater than 1000	Very Strong Support for Prosecution Hypothesis over Defense Hypothesis

*See* Ex. J to Colson Aff., OCME Forensic STR Analysis Protocol at 467. Thus, for any LR greater than one, OCME concludes that there is at least some support for the prosecution hypothesis, i.e. that the suspect's DNA is included in the mixture. When the LR value is less

than one, the OCME concludes that the mixture is better explained by the defense hypothesis.

*See id.*

The OCME began work on the development of the FST in 2008. Therese Caragine, Ph.D. and Adele Mitchell, Ph.D., headed the group of forensic scientists within the OCME who developed and validated the program. *See e.g.* Investigation into the New York City Office of Chief Medical Examiner: Department of Forensics and Biology, State of New York, Office of the Inspector General 28 (Dec. 2013), *available at* <http://ig.ny.gov/pdfs/OCMEFinalReport.pdf>. (noting that “In 2008, Adele Mitchell, a statistician, was hired to assist in developing the software, eventually known as the FST. Caragine was also instrumental in creating the FST”) (hereafter “Inspector General Report”).<sup>2</sup> *See also* Ex. K to Colson Aff., *FST Validation Study* at 759, and Ex. L to Colson Aff., Jahelda Perez, *et al.*, *Estimating the number of contributors to two-, three-, and four-person mixtures containing DNA in high template and low template amounts*, *Croat. Med. J.* 52, 314-26, 314 (2011) (hereafter “Contributor Estimate Study”) (listing Mitchell and Caragine as authors).

The DNA Subcommittee to the New York State Commission on Forensic Science issued a recommendation approving the use of FST in forensic cases in 2010. The Commission then adopted the subcommittee’s recommendation, following which OCME began using the FST in its criminal casework. *See* Ex. K to Colson Aff., *FST Validation Study* at 759. OCME did not

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<sup>2</sup> Dr. Caragine is a former Deputy Director of the Department of Forensic Biology within the OCME. *See* Inspector General Report, at 26. On April 19, 2013, Dr. Caragine resigned her position for allegedly failing to follow lab protocol, which prompted an investigation by the State of New York, Office of the Inspector General. *Id.* at 26. After the investigation, the Office of the Inspector General issued a report, finding that “in two instances, [Dr. Caragine] ignored laboratory protocol regarding resolution of scientific disputes by rewriting a final report and reassigning cases when she disagreed with the findings rather than bringing them to the DNA technical leader for arbitration.” *Id.* at 1.

provide the DNA Subcommittee with the actual FST program or with the source code for the FST prior to requesting its approval. Chakraborty Decl. ¶ 6.

Following the DNA Subcommittee's approval of the FST, in 2011 and 2012, OCME published two articles outlining the results of its validation studies on the software – the FST Validation Study and the Contributor Estimate Study. *See* Exs. K and L to Colson Aff.

Validations are the process by which labs demonstrate that their methods are robust and reliable. Chakraborty Decl. ¶ 32. Various scientific experts, including Dr. Chakraborty, have reviewed OCME's validation studies. To this day, however, OCME has still not released the source code to the FST program or made the program available for public use. *Id.* at ¶ 30.

#### 5. The OCME Reports

OCME issued four reports in connection with this case. Each is addressed separately below.

##### a. January 9, 2014 Report

OCME's initial report, dated January 9, 2014, indicates that the lab performed PCR DNA testing on three swabs from the gun: (1) the "trigger and trigger guard," (2) the "entire grip area," and (3) the "slide grip grooves." *See* Ex. C to Colson Aff. at SMALLS0092. Human DNA was extracted from each of the swabs, and they were each deemed "suitable for comparison." *Id.*

The analyst concluded that the mixture from the grip area and the slide grip grooves each contained DNA from at least three people and that the sample from the trigger and trigger guard contained DNA from at least two people. *Id.* at SMALLS0093. The individual contributors to the samples could not be determined. *Id.*

b. March 13, 2014 Report

On February 11, 2014, OCME received a court-ordered DNA exemplar from Mr. Smalls. *See Ex. E to Colson Aff. at SMALLS0226.* Later that day, following an email inquiry from OCME, NYPD Detective Laschke sent the following email in response: “Sgt Cummings would like this swab from the individual Mr. Smalls uploaded and compared to the complaint as a Suspect Swab. ‘Investigation into the case in question, where Mr. Smalls was in fact the victim of an assault (gun shot) revealed that Mr. Smalls was in possession of and discharged a firearm at another during such incident. Mr. Smalls is suspected of perpetration [of] multiple incidents within the 101<sup>st</sup> and 100<sup>th</sup> precincts. Mr. Smalls is a POI in Homicide....’” *Id.*

On March 13, 2014, an OCME analyst uploaded Mr. Smalls’ profile into their database, but could not associate his profile with any of the above three evidence items. *See id.* at SMALLS0211.

c. May 29, 2014 Report

OCME issued its third report on May 29, 2014, after securing a court-ordered DNA exemplar of Megan Woods and comparing her DNA profile to the three swabs. *See Ex. D to Colson Aff. at SMALLS0255-59.* Ms. Woods was excluded as a contributor to the DNA mixture from the trigger and trigger guard and from the slide grip grooves, but she could not be ruled out as a contributor to the mixture found on the swab from the grip area. *Id.* at SMALLS0255. Thus, a likelihood ratio was calculated using the FST. OCME concluded that it was “approximately 214 times more probable if the sample originated from three unknown, unrelated persons rather than if it originated from Megan Woods and two unknown, unrelated persons. Therefore, there is strong support that three unknown, unrelated persons contributed to this mixture, rather than Megan Woods and two unknown, unrelated persons.” *Id.*

d. June 4, 2014 Report

OCME issued its final report on June 4, 2014, documenting its comparison through the FST of Mr. Smalls' profile with the DNA evidence retrieved from the gun. *See* Ex. E to Colson Aff. at SMALLS0212-16. OCME performed two electropherogram runs on the DNA mixture from the grip area. Chakraborty Decl. ¶ 46. A table charting OCME's comparison of the runs to Mr. Smalls' DNA profile is set forth below.

	Profile	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539
J. Smalls		13, 15	28,35	11,11	11,11	15,14	7,9.3	12,12	9,11
Run One	1	10, 12, 13, 14, 15, 16	27, 28, 29, 32.2, 35	10, 11	11, 12	14, 15, 16, 17, 19	7, 8, 9.3	9, 11, 12, 13	9, 10, 11, 12
Run Two	2	12, 13, 14, 15	27, 28, 32.2	10, 11, 12	9, 10, 11, 12	14, 15, 16, 19	6, 7, 9.3	8, 9, 12, 13, 14	8, 9, 12, 13

	Profile	D2S1338	D19S433	vWA	TPOX	D18A5 1	D5A818	FGA
J. Smalls		19,24	12,14	17,19	7,8	17,20	12,12	21,24
Run One	1		12, 13, 13.2, 14, 14.2, 15	14, 15, 17, 18, 19	7, 8, 9	13, 18	11, 12, 13	21, 22, 24, 25
Run Two	2		10, 11, 12, 13, 14, 14.2, 16.2	13, 14, 15, 16, 17, 19	7, 8, 9	17	9, 11, 12, 13	21, 24

*See also* Ex. E to Colson Aff. at SMALLS0227.

As the table demonstrates, the two runs produced different results at 13 of the 15 loci examined because of allele drop-in and drop-out. *Id.* At Locus D19S433, for example, Run One identified six alleles, and Run Two identified seven alleles. Alleles 13.2 and 15, present in Run One, were not present in Run Two. Alleles 10, 11 and 16.2, present in Run Two, did not appear

in Run One.<sup>3</sup> At locus D18A5, none of Mr. Smalls' alleles (17 or 20) appeared in Run One, and only one (17) was present in Run Two. At D21S11, both of Mr. Smalls' alleles were present in the first run (28, 35), but one allele (35) did not appear in the second run. At D2S1338, no alleles were present on either run, indicating full drop-out at that locus. *Id.*

Because the two runs showed different results, OCME compared all of the alleles from both runs with Mr. Smalls' DNA profile. Chakraborty Decl. ¶ 47. The analyst then ran the FST and concluded that "[t]he DNA mixture found on the swab from 'entire grip area' is approximately 4,190 times more probable if the sample originated from Jermaine Smalls and two unknown, unrelated persons, than if it originated from three unknown, unrelated persons. Therefore, there is very strong support that Jermaine Smalls and two unknown, unrelated persons contributed to the mixture, rather than three unknown, unrelated persons." Ex. E to Colson Aff. at SMALLS0212.

Although the samples from the trigger and trigger guard and the slide grip grooves were found suitable for comparison, the analyst did not perform the FST on these samples. Instead, the analyst performed additional electropherogram runs on the evidence from the trigger and trigger guard, and excluded Mr. Smalls as a contributor to that sample. Ex. C to Colson Aff. at SMALLS0121-22; Ex. E to Colson Aff. at SMALLS0213. In addition, the analyst compared the number of alleles seen in Mr. Smalls' profile with the alleles seen in the mixture from the slide grip grooves and concluded that "it cannot be determined whether they [Mr. Smalls' alleles] can or cannot be excluded as a contributor to the [slide grip grooves] mixture." Ex. E to Colson Aff. at SMALLS0212.

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<sup>3</sup> A total of nine alleles were observed from both runs at Locus D19S433. Assuming that each person has a maximum of two alleles, this indicates that at least four people contributed to that locus, unless there was significant drop-in. *Id.*

### III.

#### THE DAUBERT STANDARD

Federal Rule of Evidence 702 allows for the admissibility of expert testimony so long as “(1) the testimony is based upon sufficient facts or data, (2) the testimony is the product of reliable principles and methods, and (3) the expert has applied the principles and methods reliably to the facts of the case.” Fed. R. Evid. 702. The district court has a “gatekeeping” function under Rule 702, and is charged with “ensur[ing] that any and all scientific testimony or evidence admitted is not only relevant, but reliable.” *Daubert*, 509 U.S. at 589.

As part of its gatekeeping function, the district court must make a “preliminary assessment of whether the reasoning or methodology underlying the testimony is scientifically valid and of whether that reasoning or methodology properly can be applied to the facts in issue.” *Daubert*, 509 U.S. at 592-93. The Supreme Court has identified a number of factors bearing on reliability that district courts may consider, such as: (1) whether a theory or technique “can be (and has been) tested;” (2) whether the theory or technique “has been subjected to peer review and publication;” (3) a technique’s “known or potential rate of error;” and the “existence and maintenance of standards controlling the technique’s operation;” and (4) whether a particular technique or theory has gained “general acceptance” in the “relevant scientific community.” *Id.* at 593-94; *see also Amorgianos v. Nat’l R.R. Passenger Corp.*, 303 F.3d 256, 266 (2d. Cir. 2002).

These factors are not a “definitive checklist or test.” *Daubert*, 509 U.S. at 594. Rather, the *Daubert* inquiry is “fluid” and “will necessarily vary from case-to-case.” *Amorgianos*, 303 F.3d at 266. The Court has “considerable leeway” in “deciding how to test an expert’s reliability, and to decide whether or when special briefing or other proceedings are needed to investigate reliability.” *Kumho Tire Co. v. Carmichael*, 526 U.S. 137, 152 (1999).

“To warrant admissibility...it is critical that an expert’s analysis be reliable at every step.” *Amorgianos*, 303 F.3d at 267. Further, an expert’s conclusions must be “supported by good grounds for *each step* in the analysis” and “*any step* that renders the analysis unreliable under the *Daubert* factors renders the expert’s testimony inadmissible.” *Id.* at 267 (internal citations and quotations omitted) (emphasis added); *see also Heller v. Shaw Indus., Inc.*, 167 F.3d 146, 155 (3d Cir. 1999) (“[T]he reliability analysis applies to all aspects of an expert’s testimony: the methodology, the facts underlying the expert’s opinion, the link between the facts and the conclusion, *et alia.*”)

Thus, “when an expert opinion is based on data, a methodology, or studies that are simply inadequate to support the conclusions reached, *Daubert* and Federal Rule of Evidence 702 mandate the exclusion of that unreliable opinion testimony.” *Amorgianos*, 303 F.3d at 266. The same is true when a reliable methodology is changed or misapplied in a particular case. *See In re Paoli R.R. Yard PCB Litig.*, 35 F.3d 717, 745 (3d Cir. 1994) (“any step that renders the analysis unreliable under the *Daubert* factors renders the expert’s testimony inadmissible. This is true whether the step completely changes a reliable methodology or misapplies that methodology.”)

In addition, while the thrust of the *Daubert* inquiry is on scientific methodology, the conclusions drawn by the expert are also relevant. The Supreme Court has stated:

[C]onclusions and methodology are not entirely distinct from one another....[N]othing in either *Daubert* or the Federal Rules of Evidence requires a district court to admit opinion evidence that is connected to existing data only by the *ipse dixit* of the expert. A court may conclude that there is simply too great an analytical gap between the data and the opinion proffered.” *General Electric Co. v. Joiner*, 522 U.S. 136, 146 (1997).

Finally, in assessing the admissibility of expert evidence, a district court should be mindful of other applicable rules, including Federal Rule of Evidence 403, which permits the exclusion of evidence if its “probative value is substantially outweighed by the danger of...unfair

prejudice, confusion of the issues, or misleading the jury....” *Daubert*, 509 U.S. at 595; Fed. R. Evid. 403. Courts have noted the potential “mystic infallibility” of scientific evidence, particularly DNA evidence. *United States v. Williams*, 583 F.2d 1194, 1199-1200 (2d Cir. 1978), *cert. denied*, 439 U.S. 1117 (1978). *See also United States v. Jakobetz*, 747 F.Supp. 250, 262 (D. Vt. 1990) (“Arguably, DNA profiling is particularly capable—in more ways than one—of lulling a jury into slumbering at its post and not rigorously sifting the evidence.”) Because “[e]xpert evidence can be both powerful and quite misleading ... the judge in weighing possible prejudice against probative force under Rule 403...exercises more control over experts than over lay witnesses.” *Daubert*, 509 U.S. at 595. (citation omitted).

As the proponent of the expert evidence, the government bears the initial burden of proving reliability and relevance by a preponderance of proof. *Liberty Media Corp. v. Vivendi Universal*, 874 F.Supp. 2d 169, 172 (SDNY 2012). The government cannot meet its burden here.

#### IV.

#### ARGUMENT

Traditional DNA typing has become a mainstay of forensic science. Hundreds of law enforcement laboratories in the United States perform and utilize standard STR/PCR DNA testing in criminal cases, and both state and federal courts universally recognize the reliability of STR/PCR DNA testing and admit the results.

The statistical evaluation of DNA mixtures, by contrast, is a relatively new field, and the forensic DNA community is still trying to pave a path forward. In recent years, various software programs have emerged for computing LR<sub>s</sub> with DNA mixtures. These programs are each in differing stages of development; they each employ a different statistical model; and they each

generate differing results. *See* Ex. Q to Colson Aff., Christopher D. Steele and David J. Balding, *Statistical Evaluation of Forensic DNA Profile Evidence*, *Annu. Rev. Stat. Appl.* 2014, 1:361-84, at 381 (hereafter “*Statistical Evaluation*”); *see also* Ex. R to Colson Aff., Hinda Haned, *et al.*, *Complex. DNA mixture analysis in a forensic context: Evaluating the probative value using a likelihood ratio model*, *Forensic Sci. Int’l: Genetics* 16, 17-25, 17 (2015) (hereafter “*Complex. DNA mixture analysis*”) (“In recent years ... a number of new computer programs have been introduced. These software are anchored in a likelihood-ratio model, but they all use different probabilistic models, and rely on different distributional assumptions.”)

OCME is the *only* laboratory in the world that performs and utilizes the FST. The methodology underlying the FST is unique, and its reliability is a disputed topic in the scientific community and in courtrooms.

To our knowledge no federal court has ever admitted FST evidence in support of a defendant’s guilt, and there have been no reported decisions relating to *Daubert* challenges of the FST. Recently, the Honorable Mark Dwyer excluded the introduction of FST evidence in two combined criminal cases in Kings County Supreme Court because the program has not been generally accepted in the scientific community. *See* Ex. F. to Colson Aff., *People v. Peaks & Collins*, Sup Ct, Kings County, Nov. 7, 2014, Dwyer, J., Ind. Nos. 80077-2010, 7690-2010, at 6 (“the dissenting chorus was strong enough that I can’t say that the *Frye* test has been satisfied.”) The Court’s decision followed an extensive evidentiary hearing, which took place over the course of a year and included testimony from eleven experts.

The only state court to have admitted the FST following an evidentiary hearing, *see People v. Rodriguez*, Sup Ct, NY County, Oct. 24, 2013, Caruthers, J., Ind. No. 5471-2009, found that likelihood ratios “have long been generally accepted by forensic scientists as reliable.”

*See id.* at 7. This may be true. But the Court’s reasoning in *Rodriguez* is nonetheless flawed. The primary question is not whether likelihood ratios are accepted in other settings. The question is whether OCME’s *application* of a likelihood ratio here—using pre-set drop-out and drop-in rates—is reliable and generally accepted by the relevant scientific community. *See Paoli*, 35 F.3d at 745 (“any step that renders the analysis unreliable under the *Daubert* factors renders the expert’s testimony inadmissible. This is true whether the step completely changes a reliable methodology or misapplies that methodology.”) *See also* Ex. P to Colson Aff., Hinda Haned, *et al.*, *Exploratory data analysis for the interpretation of low template DNA mixtures*, *Forensic Sci. Int’l: Genetics* 6, 762-74, 773 (2012) (hereafter “*Exploratory data analysis*”) (“likelihood ratios rely on the model used to generate them”). The answer to this question is no. Since the FST’s final LR depends on the drop-out values being input into the calculation, errors associated with the drop-out estimate directly impact the reliability and general acceptance of FST. As discussed below, the errors are numerous, and their combined effect renders the FST inadmissible under *Daubert*.

#### A.

##### **The Methodology Used to Develop the Drop-Out Rate is Flawed, Leading to Unreliable Results**

##### 1. Using DNA Quantity to Determine the Drop-Out Rates is Unique and Unproven

The FST’s methodology is unique in that it utilizes pre-determined allele drop-out and drop-in rates based on DNA quantitation. OCME’s main assumption is that the drop-out and drop-in rates may be determined based on the amount of DNA in a sample. Ex. K to Colson Aff., *FST Validation Study* at 756. No other lab or program in the world ascribes to this hypothesis. *See* Ex. H to Colson Aff., Testimony of Dr. Eli Shapiro, *People v. Peaks & Collins*, 10/15/2013, at 177 (“Yes, I think the entire approach of the FST, which is a very unique one, and

I think the only one in the field, is to use the quantitation values, for a sample, in order to determine the drop-out rates to apply to the mixture.”); *see also* Ex. I to Colson Aff., Testimony of Dr. Bruce Budowle, *People v. Peaks & Collins*, 12/9/2013, at 793 (The FST “makes certain assumptions about DNA typing that no one else would do even in all standard DNA typing. The main assumption being made is that all the rates for drop-in, drop-out are based on the amount of the DNA....”) <sup>4</sup>

There are various competing LR ratio programs, including *LoComationN*, *Forensim*, *True Allele*, *likeLTD*, *STR Mix*, *Armed Xpert*, and *LabRetriever*. Unlike the FST, however, none of these programs arrives at pre-determined drop-out rates based on DNA quantity. Rather, they allow the user to input a range of drop-out rates based on the specific features of a case, or they focus on the average peak heights at the allelic positions. <sup>5, 6</sup> In short, each of these programs rejects the FST’s pre-set drop methodology. *See, e.g.*, Ex. S to Colson Aff., David J. Balding and John Buckelton, *Interpreting low template DNA profiles*, *Forensic Sci. Int’l: Genetics* 4, 1-10, 5 (2008) (creators of *likeLTD* arguing that “DNA-based prosecutions that rely on drop-out

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<sup>4</sup> The complete testimonies of three testifying experts, Dr. Eli Shapiro, Dr. Bruce Budowle, and Dr. Ranajit Chakraborty are attached to the Colson Affirmation for the Court’s review. We also have a copy of the entire *Peaks/Collins Frye* hearing transcript should the Court wish to see it.

<sup>5</sup> *Forensim* and *LoComationN* allow the user to specify drop-out and drop-in probabilities. Ex. K to Colson Aff., *FST Validation Study* at 750. *Forensim* then calculates the LR for a range of drop-out rates and displays the results graphically. *Id.* *See also* Ex. Q to Colson Aff., *Statistical Evaluation* at 378. *LikeLTD* finds the drop-out probabilities and mixtures that maximize the LR under the prosecution and defense hypotheses. Ex. K to Colson Aff., *FST Validation Study* at 750. *TrueAllele* uses electropherogram peak heights at every allelic position without taking drop-out into account. *See* Ex. Q to Colson Aff., *Statistical Evaluation* at 379. And *LabRetriever* uses peak heights and allows the analyst to vary the drop-in and drop-out rates based upon the evidence. *See Rodriguez*, Sup Ct, NY County, Oct. 24, 2013, Caruthers, J., slip op. at 44-45.

<sup>6</sup> For his part, Dr. Chakraborty believes that each of these programs has its benefits and drawbacks. But the research in this area is still in its infancy, and none of these programs, including the FST, is ready for use in court. Chakraborty Decl. ¶ 28.

and do not explicitly estimate plausible ranges for the drop-out rate parameter, are in our view, defective.”); Ex. P to Colson Aff., *Exploratory data analysis* at 768 (creators of Forensim suggesting the use of a range of drop-out rates based on the crime scene sample itself with the advantage being “that the ranges of the drop-out probability can be evaluated separately under  $H_p$  and  $H_d$ , and that we avoid reporting values of drop-out that are supported by one hypothesis but not by its alternatives.”)

Shockingly, despite its novel approach, OCME has never adequately tested its most critical assumption, i.e. that drop-out rates consistently correlate with DNA quantity. Dr. Adele Mitchell, one of the lead developers of the FST, recently testified that she: (1) never conducted a formal study to test the effect that changing the quantity of DNA could have on LR<sub>s</sub>; (2) did not publish her informal testing in any validation studies or other scientific articles; (3) never presented her testing to the DNA Subcommittee; and (4) did not show her work to anyone outside the OCME, or even to her supervisor inside the OCME. See Ex. M to Colson Aff., Testimony of Dr. Adele Mitchell, *People v. Peaks & Collins*, 5/21/13, at 28-32. In other words, Dr. Mitchell has insufficient evidence to support the most basic premise of the FST.

Correlating drop-out rates with DNA quantity is thus both unique *and* unproven. Absent the performance and disclosure of studies documenting the validity of OCME’s approach, the FST fails the testing requirement under *Daubert*. See *In re TMI Litig*, 193 F.3d 613, 674-75 (3d Cir. 1999) (holding expert testimony inadmissible because a crucial part of the analysis was a study that was never performed); *Daubert*, 509 U.S. at 593-95 (whether a theory or technique “can (and has been) tested” is a key factor bearing on reliability.) For this reason alone, the FST evidence should be excluded.

## 2. Using DNA Quantity to Determine Drop-Out is Prone to Error

OCME's failure to test whether drop-out consistently correlates with DNA quantity is not the only problem with the FST. Dr. Theresa Caragine, another lead developer of the FST, has admitted that OCME's method of quantifying DNA has a 30% error rate. Ex. N to Colson Aff., Testimony of Dr. Theresa Caragine, *People v. Peaks & Collins*, 12/12/2012, at 41 ("The accuracy is within thirty percent of the expected value, which is much more accurate than commercial tests.") Despite this admission, OCME has not published any studies explaining how the error rate may affect the reliability of the FST. Chakraborty Decl. ¶ 31.

Moreover, while OCME claims its quantitation method is more accurate than that of the wider industry, it is not accurate enough for the purpose for which it is used in the FST. Quantity measure does not have to be that accurate for the amplification step of traditional DNA typing because, during amplification, it is possible to immediately discern whether a sufficient quantity of DNA was used and to correct for possible error. *See* Ex. H to Colson Aff., Shapiro Test., 10/15/2013, at 183. But a 30% range of error is unacceptable for use in estimating drop-out rates. Chakraborty Decl. ¶ 31. This is because the FST comparison generates only *one* statistical value, and there are no opportunities to assess and correct any errors made during the process. *Id.*

In addition, within the framework of FST, there is no way to determine the proportion of each contributor's DNA to a DNA mixture. Thus, for DNA mixtures, the use of a single DNA quantity to estimate drop-out rates correlates little, if at all, with the drop-out rates for individual contributors. *Id.*

OCME's failure to test or identify how the 30% error rate in quantitation impacts the LR compounds the uncertainty inherent in using quantity to determine the drop-out rate. Together,

these failings undermine the program's reliability under two *Daubert* factors, including whether the methodology has been adequately tested and whether the actual relevant error rate is known.

*See Daubert*, 509 U.S. at 594.

3. The OCME's Validation Studies Fail to Consider the Complex Features of Real-World Crime Scene Samples

On their face, the OCME's validation studies appear to rest on sound science. OCME claims to have performed a large number of experiments; it has documented some of its findings; and it appears to have developed a tool consistent with those findings. But good science requires the rigorous testing and examination of assumptions and the willingness to perform additional studies and testing when initial assumptions are not borne out by the evidence or lack real-world application. The OCME falls far short of meeting these standards.

One of the most concerning features of the OCME validation studies is their failure to consider the unique features of real-world crime scene samples. The DNA samples OCME examined in its validation studies were extracted from "pristine buccal swabs." Ex. K to Colson Aff., *FST Validation Study* at 756.<sup>7</sup> ("The samples used for the current analysis were pristine buccal swabs.") By contrast, DNA extracted from evidence in the field is often degraded because of exposure to dirt, bacteria, or sunlight. Chakraborty Decl. ¶ 25. Indeed, as discussed more fully in sub-section E below, the DNA extracted from the grip area of the gun in this case was heavily degraded.

In addition, OCME assumed a very small number of possible mixture ratios for contributors to DNA samples. Ratios of 1:1 and 4:1 were used for two-person DNA mixtures;

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<sup>7</sup> Interestingly, OCME reports having tested 104 touched samples, but it does not report the results separately, nor does it present the drop rates or the false positive and false negative rates for touched items. *See* Ex. K to Colson Aff., *FST Validation Study* at 752 (noting that 104 touch samples were used); Ex. H to Colson Aff., Shapiro Test., 10/4/13, at 72 ("They did not show in validation that I can see a curve or a graph or table that they show what were the likelihood ratios they obtained using degraded samples and what were the likelihood ratios using pristine values.")

ratios of 1:1:1 and 5:1:1 were used for three person DNA mixtures. *See* Ex. K to Colson Aff., *FST Validation Study* at 753. In the real world, however, the proportions of DNA each person contributes to a mixture are unknown and unlikely to conform to those derived from the validation studies. Chakraborty Decl. ¶ 32; *see also* Ex. H to Colson Aff., Shapiro Test., 10/4/13, at 65 (“The actual ratios in the mixtures in real casework basically would almost never conform to those present models.”)

Finally, the studies ignored the possible relatedness of the contributors to each other or the suspect, and the effect relatedness may have on allele drop-out. Ex. K to Colson Aff., *FST Validation Study* at 759 (the FST calculation is based on unrelated individuals); Ex. C to Colson Aff. at SMALLS0096 (“statistical values reported reflect the approximate frequency of occurrence of a DNA profile in a population of unrelated individuals. Therefore, they are not appropriate for relatives.”) But relatedness is often an issue in real criminal cases. Related individuals commonly share touched items, like door knobs and bicycle handlebars. And, of course, the possibility of relatedness is often a part of the defense hypothesis.

Importantly, OCME acknowledges that degradation and relatedness may affect drop-out rates, and that further testing of these features is warranted. *See, e.g.*, Ex. K to Colson Aff., *FST Validation Study* at 756 (“The samples used for the current analysis were pristine buccal swabs. Results may differ if samples displaying (stet) more of the complicated characteristics of many evidence samples. Further study of these phenomena is warranted.”); *id.* at 759 (Further testing on degraded DNA samples is “warranted, as improvement in quantification of degradation or identification of moderately to severely degraded samples coupled with changes to the degradation model might improve performance.”); Ex. L to Colson Aff., *Contributor Estimate Study* at 325 (“Consequently, touched items displayed a wider range of the number of different

alleles than purposeful mixtures indicating that there was more allele drop-out and drop-in.”); Ex. K to Colson Aff., *FST Validation Study* at 760 (“There are two main limitations to the current version of the FST application. First, correlation among genotypes of contributors to mixtures is not considered...”)

In addition scientific experts highly respected in the field of forensic DNA identification have criticized OCME’s failure to test and account for case-specific variables. Drs. Eli Shapiro,<sup>8</sup> Bruce Budowle,<sup>9</sup> and Ranajit Chakraborty<sup>10</sup> are among the leading critics of OCME’s methodology. All three experts agree that degradation, mixture ratios, and relatedness can alter drop-out rates on a case-specific basis and thus affect the range of reasonable LR’s. *See* Ex. I to Colson Aff., Budowle Test., 12/9/2013, at 822 (“The concept of using total DNA is – actually makes no sense...[because] we see from real casework the outcome is not consistent, it depends on the quality of the DNA, if it’s degraded, if it’s got inhibitors, these sorts of things.”); Ex. H to Colson Aff., Shapiro Test., 10/4/13, at 64-65 (“Then when it’s going to assign...a specific number of contributors to the mixture based on sort of preset criteria, without considering that

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<sup>8</sup> Dr. Shapiro is a former assistant director at the Department of Forensic Biology at the OCME. He was the director of training there for roughly 10 years and leader of the Mitochondrial Team. He is a graduate of Columbia and Yale Universities. Colson Aff. ¶ 12.

<sup>9</sup> Dr. Budowle is a former senior scientist and lab head with the FBI, where his career spanned more than 25 years. His work was critical to developing the Combined Offender DNA Index System (CODIS). Colson Aff. ¶ 13.

<sup>10</sup> Dr. Chakraborty is a professor in the Department of Molecular and Medical Genetics and the Director of the Center for Computational Genomics at the Institute of Applied Genetics at the University of North Texas Health Science at Fort Worth, Texas. Chakraborty Decl. ¶ 1. He is a preeminent population geneticist. Dr. Chakraborty helped to develop the 13 core STR genetic markers used by the FBI and in labs throughout the world. *Id.* at ¶ 4. Dr. Chakraborty was a member of the DNA subcommittee that approved the FST in 2010. *Id.* at ¶ 7. Since voting for these methodologies, however, he has developed serious concerns about the use of the FST based on additional research and developments in the field, particularly in relation to complex cases. *Id.*

there could be degradation, that there could be different numbers of contributors at different locations in the DNA but...larger and smaller locations....It doesn't...really count for all the different ratios of contributors that are possible and could be suggested by the actual evidence."); Chakraborty Decl. ¶ 32. *See also* Ex. T to Colson Aff., Peter Gill and Hinda Haned, *A new methodological framework to interpret Complex DNA profiles using likelihood ratios*, Forensic Sci. Int'l: Genetics 7, 251-263, at 262 (2013) (hereafter "*A new methodological framework*") ("generalisation [sic] across the entire possible range of casework examples that may be encountered is unrealistic to achieve. Therefore the development of case-specific performance measures is needed to evaluate a likelihood ratio.")<sup>11</sup>

Despite OCME's own admissions of weaknesses in the FST program, and the valid criticisms of leading experts, to this day, OCME has not published any additional studies documenting how case-specific variables may affect the LR. Chakraborty Decl. ¶ 33. Nor has OCME made any documented adjustments to the FST program. *Id.* To our knowledge, OCME simply continues to use the pre-set rates, based on validation studies from pristine buccal swabs, with a minimal number of mixture ratios, and the DNA of unrelated individuals.

This is nothing short of unacceptable. OCME is a public laboratory tasked with analyzing evidence in thousands of serious cases each year. Features such as degradation, varying mixture ratios, and relatedness do not just impact the rare DNA case. One or more of these features is

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<sup>11</sup> The current FST method of using pre-set criteria also fails to include a process for testing the false positive rate on a case-by-case basis. Leading scientists have rejected this approach, advocating for case-specific non-contributor performance testing to assess the weight of the evidence. *See, e.g.,* Ex. T to Colson Aff., *A new methodological framework* at 261 ("Interrogation with non-contributor performance tests...can be used to demonstrate the performance of the model. It is proposed here that performance tests also serve the purpose of validation on a per case basis...by providing a concurrent risk analysis. This flexibility is a desirable feature of any complex theory, since it is impossible to generalize across the entire range of propositions/profiles that may be encountered.")

likely to impact *every* criminal case involving DNA mixtures. Chakraborty Decl. ¶ 32. Since the effect of these features has never been validated, the LR<sub>s</sub> generated by the FST have no real-world application. They are unreliable and should be excluded under *Daubert*. Cf. *Reed Construction Data, Inc. v. The McGraw-Hill Cos., Inc.*, No. 09-CV-8578, 2014 WL 4746130, (SDNY Sept. 2014) (“to be admissible, a [statistical] regression analysis must control for the ‘major factors’ that might influence the dependent variable.”) (citation omitted); *Medisim Ltd v. Bestmed LLC*, 861 F.Supp.2d 158, 166 (SDNY 2012) (“[T]he closer the survey methods mirror the situation in which the ordinary person would encounter the trademark, the greater the evidentiary weight of the survey results. The failure of a survey to approximate actual marketplace conditions can provide grounds for inadmissibility.”) (citation and internal quotation marks omitted.)

4. The FST Assumes Independence of Drop-Out Rates Across Alleles Without Proper Validation

As part of its presentation to the DNA Subcommittee, the OCME submitted a summary of its validation studies as to the possible dependence of alleles across loci. In the summary, OCME concluded that drop-out rates appear to be independent across loci. See Ex. B to Chakraborty Decl. ¶ 35, Likelihood Ratio Statistics For Analysis of Single Source, Mixed and Degraded Evidence Samples, Volume 22: Determination of Independence of Drop-Out Among Loci, Summary at 1. (“Drop-out rates appear to be independent across loci. That is, drop-out or lack of drop-out at each locus is not consistently associated with an increased or decreased probability of drop-out at other loci.”); Chakraborty Decl. ¶ 35. In other words, the OCME assumes that there is no correlation between drop-out at one locus and drop-out at other loci.

Dr. Chakraborty has examined the underlying data and has determined that it does not support this conclusion. Chakraborty Decl. ¶ 35. First, OCME disregards its own data.

Attached to its summary conclusions, OCME included tables reflecting OCME's statistical analysis, which showed that some positive and negative correlations between drop-out rates at different loci were observed but were not consistent. *See* Ex. B to Chakraborty Dec., Summary at 3 ("Within each set of mixtures, drop-out at some loci was associated with drop-out (or lack of drop-out) at other loci. However, these associations were not consistent across the mixtures, indicating that there is no consistent correlation in drop-out probability among loci."); *see also* Chakraborty Decl. ¶ 35. Rather than trying to account for the complexities in the correlations or further studying them, OCME reached a conclusion inconsistent with the data - that the drop-out rate across loci is independent.

Second, the data set used by OCME to reach its conclusion was limited and does not account for all of the real-life factors that could influence the dependence or independence of drop-out rates across loci. These include the varying number of contributors, allele sharing between them, varied mixtures ratios, and uneven degradation of the DNA. Chakraborty Dec. ¶ 36. Nor did OCME factor its failure to consider these variables into its calculation of drop-out rates.

Third, the OCME's testing of drop-out across loci was too simplistic. OCME chose one locus, and asked whether drop-out rates there were consistent with drop-out at other loci under various conditions. Instead, it should have considered whether drop-out rates of all 15 loci were simultaneously independent of each other. Chakraborty Decl. ¶ 37.

Dr. Chakraborty has recommended that OMCE complete further studies on the dependence of drop-out across loci. Chakraborty Decl. ¶ 38. To date, however, the OCME has not published any studies showing whether and/or how such additional work has been done or factored into the FST. *Id.* Without an accurate assessment of the dependence/independence of

drop-out rates, the LR ratios generated by the FST have no scientific value, and should be excluded under *Daubert*.

5. The Racial Identities of the Contributors to the Validation Studies Were Not Preserved, Making it Impossible to Verify Whether Racial Identity Was Properly Considered in Formulating Drop-Out Rates

In their validation studies, the OCME tested 439 mixtures. *See* Ex. K to Colson Aff., *FST Validation Study* at 752 (noting that 454 mixtures and touched items were included in the validation, 15 of which were only from a single source.) Their published validation studies described the racial background of contributors to the mixtures as follows:

The 85 contributors represented the diverse population of New York City. For 72% of the samples, the ethnicity of the donor was known, as these donors were laboratory employees. The breakdown was as follows: 20% Asian, 16% Black, 54% Caucasian, and 10% Hispanic. The remaining samples were obtained at autopsy and represented a random draw from the population of New York City. According to the 2010 United States census, the population of New York City is 9.8% Asian, 26.6% black, 44.7% Caucasian, and 27% Hispanic. *Id.* at 753.

Despite describing the racial composition of the contributors to the mixtures in their validation studies, the OCME did not preserve its data about the racial characteristics of the contributors for review and validation by other scientists. Chakraborty Decl. ¶ 40. *See also* Ex. O to Colson Aff., Testimony of Mimi Mairs, *People v. Peaks & Collins*, 6/17/13, at 9 (Mimi Mairs, Special Counsel, Forensic Biology at OCME stating in response to court's inquiry about availability of racial data underlying the FST study: "Doctor Mitchell states that she and, Doctor Carajine [sic] tallied up on a piece of scratch paper and that piece of scratch paper was not saved so when I say that there is no document much less a formal document, there is none.") Nor did the OCME provide data concerning the racial identifications or subpopulations of the contributors to the mixtures to the DNA Subcommittee that approved the FST's use. Chakraborty Decl. ¶ 40.

Racial and subpopulation characteristics are critical to an accurate determination of drop-out rates, and this data should have been preserved for external review. Dr. Chakraborty has explained that allele frequency is an important possible predictor of drop-out rate, and allele frequency varies by race and ethnicity, with members of the same race and ethnicity sharing more alleles. Chakraborty Decl. ¶ 39; Chakraborty Test., 12/16/13 at 1119-20. *See also* Ex. I to Colson Aff., Budowle Test., 12/10/2013, at 921 (“if you take two people who are Caucasians, they are more likely to share alleles amongst them, just being Caucasians....If you take two Africans, they have a better chance of sharing two alleles in common because they have certain ones more common. So, you get -- it would be different alleles that are more common in one population than another.”) In Dr. Chakraborty’s expert opinion, if race and ethnicity are not properly accounted for, the drop-out rates will be unreliable. Chakraborty Decl. at ¶ 39.<sup>12</sup>

The lack of transparency as to the manner in which the drop-out rate factored in race and subpopulations materially undermines the reliability of the FST under a number of *Daubert* factors, including whether the theory or technique has been tested and subjected to peer review and whether it has a known rate of error.

## B.

### **The Likelihood Ratios Generated by FST Often Prejudice the Defense**

One effect of correlating drop-out with DNA quantity is that there is no opportunity to propose alternative assumptions for the prosecution and defense hypotheses. There is only one drop-out rate, and it is held constant between the hypothesis that the defendant was involved and the hypothesis that he was not. *See* Ex. K to Colson Aff., *FST Validation Study* at 757 (“[W]e

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<sup>12</sup> Dr. Chakraborty has also explained that racial identification of the contributors to mixtures would be important in assessing the false positive rate. *See* Ex. G to Colson Aff., Chakraborty Test., 12/16/13, at 1120. Therefore, the absence of racial identification data also calls into question the reliability of OCME’s assessment of the appropriate false positive rate.

elected to empirically estimate drop-out rates as a function of the total amount of template DNA in a sample, the estimated number of contributors to the sample, their approximate ratio (equal or not equal) and STR locus.”) While OCME argues that this approach is “conservative,” the truth is this method can and does increase the LR in certain cases. *Id.* at 752.

OCME purports to adjust for potential prejudice to the defense by intentionally underestimating the drop-out rate and assuming the minimum number of contributors to a sample. *See* Exhibit K to Colson Aff., *FST Validation Study* at 752 (“In order to be conservative, FST uses the drop-out rate estimate minus one standard deviation for each locus, template DNA quantity, number of contributors, and ratio for mixed samples.”) Neither adjustment, however, has the desired effect.

#### 1. Holding the Drop-Out Rate Constant Can Prejudice the Defense

Other developers of drop models allow for varying the drop-out rate between the numerator and the denominator. Hinda Haned and Peter Gill, for example, have developed an exploratory model that allows the application of different drop-out probabilities to different contributors, and the use of different parameters under the prosecution and defense hypotheses. In a 2012 article discussing their model, Haned and Gill explained that “varying the probabilities of drop-out between the two hypotheses,  $H_p$  and  $H_d$ , led to dramatic changes in the LRs. This shows that the chosen values for the probabilities of drop-out are a very critical part of the implementation of the model in casework.” Ex. P to Colson Aff., *Exploratory data analysis* at 773.

One reason Haned and Gill consider variation in the drop-out rate as critical to their model is that holding the rate constant can prejudice the defense. During his testimony at the *Peaks/Collins Frye* hearing, Dr. Budowle demonstrated that maintaining the same drop-out rate

in both the numerator and denominator generated a higher LR at least some of the time. Moreover, increasing the drop-out rate in the denominator often lowered the LR. *See* Ex. I to Colson Aff., Budowle Test., 12/9/2013, at 830-31 (“there is a point...as you lower the drop-out rate, [the LR is] eventually going to get low but there is a certain sweet point where it will be higher. If the drop-out is higher it will be a sweet point and give a more conservative value. There is a certain point where it’s very high, it will go in the opposite direction. So, it all depends on a case by case basis what the effect is.”)

Given the potential prejudicial effect of holding the drop-out rate constant, Dr. Budwole advised: “[I]f the prosecution forms and controls the conditions for the prosecution’s hypothesis, the defense should be able to form at least reasonable hypotheses based on what the evidence is on the validation studies. So if you can’t adjust the drop-in and drop-out rates based on data, then that’s not an appropriate thing to do.” Ex. I to Colson Aff., Budowle Test., 12/9/13, at 912. *See also A New Methodological Framework* at 261 (noting that a necessary feature of any LR model is that it “must be able to determine numeric strength of evidence that favours defence or prosecution hypotheses.”)

2. There is No Empirical Evidence that Underestimating the Drop-Out Rate is Conservative

OCME purports to adjust for any potential prejudice that results from holding the drop-out rate constant by intentionally underestimating the drop-out rate. But nowhere does OCME demonstrate how or why this works. Dr. Mitchell testified during the *Peaks/Collins Frye* hearing that she never conducted a formal study on the underestimation of drop-out rates, but instead tested the proposition informally “on my own.” Ex. M to Colson Aff., Dr. Mitchell Test., 5/1/13, at 117. She further acknowledged that she did not publish the results and does not know whether

she even saved them. *Id.* Nor were the results of her informal testing summarized for the DNA Subcommittee. Chakraborty Decl. ¶ 43.

Importantly, Dr. Chakraborty has examined the available data and determined that it does not support OCME's assumption. Indeed, his review of OCME's "Study 3C" shows that underestimating drop-out rates only leads to a lower LR half the time. Chakraborty Decl. ¶ 43. As Dr. Chakraborty put it during his testimony at the *Peaks/Collins Frye* hearing, underestimating drop-out "is as good as tossing a coin." *See* Ex. G to Colson Aff., Testimony of Dr. Ranajit Chakraborty, 12/16/2013, at 1127. Half the time it will favor the prosecution, and half the time it will favor the defense.

OCME's failure to formally test its assumption, and Dr. Chakraborty's expert critique, both undermine the reliability of the FST methodology under *Daubert*.

### 3. Assuming the Minimum Number of Contributors Prejudices the Defense

OCME admits that "precise accuracy rates for estimating the number of contributors cannot be calculated." Ex. L to Colson Aff., *Contributor Estimate Study* at 324. It thus assumes the minimum number of contributors to a sample, which it also claims produces the lowest LR. *Id.* at 315 ("In other words, for a given prosecution hypothesis, using the defense hypothesis with the minimum number of possible contributors will usually result in the lowest possible LR...."); *see also* Ex. K to Colson Aff., *FST Validation Study* at 759 ("using the minimum number of contributors typically results in the lowest possible LR, the LR that most favors the defendant.")

But this disregards the substantial risk that underestimating the number of contributors will actually increase the LR, prejudicing the defense. Even OCME acknowledges "a 'moderate risk' of a non-minimal LR when the defense hypothesis with the minimum number of contributors is used." Ex. L to Colson Aff., *Contributor Estimate Study* at 316. Moreover,

leading scientific experts have shown that underestimating the number of contributors can result in higher LR's in a significant number of cases. For instance, in *A new methodological framework*, Gill and Haned presented a case study involving two suspects in a sexual assault, both of whom denied the offense. *See* Ex. T to Colson Aff., *A new methodological framework* at 255-256. When the mixture was treated as having two contributors, the LR for one of the suspects was much higher than it was if three contributors were assumed. *See id.* at 256. Thus, the choice of three contributors over two was “demonstrably conservative.” *Id.*

Experts have further shown that the risk of higher LR's increases as the number of contributors to a DNA mixture increases. *See* Ex. R to Colson Aff., *Complex DNA mixture analysis* at 22 (In tests performed, underestimating the number of contributors led to more conservative LR's in 85% of three-person samples, 56% of four-person samples, and 49% of five-person samples.) Thus, the greater the number of contributors to a sample, the greater the possibility that underestimating the number will prejudice the defense. This, too, undermines the reliability of the FST model under *Daubert*.

In short, whatever the purported merit of using quantity to estimate pre-set drop-out rates, the FST's system of fixed parameters often results in a higher LR, thereby prejudicing the defense. This methodology is not generally accepted in the scientific community and should be excluded under *Daubert*.

### C.

#### **The FST Has Not Been Subjected to Adequate Peer Review**

As discussed above, scientific experts cannot adequately test the validity of the FST because OCME refuses to disclose critical studies in support of its most fundamental assumptions. The missing, or non-existent, studies include: (1) studies testing whether drop-out

rates consistently correlate with DNA quantity, (2) studies testing how the 30% error rate in quantitation affects the LR, (3) studies testing how the unique features of real-world crime scene samples affect drop-out rates and the LR, (4) studies testing whether the drop-out rate across loci is dependent or independent, and (5) studies testing how underestimation of the drop-out rate affects the LR.

Not only has OCME failed to perform and/or disclose critical studies, it has also refused to provide forensic scientists with the source code for the FST. “Source code is the human readable form of a programming language and contains the complete set of instructions for how a computer processes input data.” Ex. U to Colson Aff., A. Morin, *et al.*, *Shining Light Into Black Boxes*, *Science*, Vol. 336, 13 April 2012, p. 159. In the absence of source code, it is virtually impossible to test the reliability of the FST program. *Id.* (“In the absence of source code, the inner workings of a program cannot be examined, adapted, or modified.”); *see also* Chakraborty Decl. ¶ 30 (“Without knowing the source-code, it is virtually impossible to test the reliability of the LR calculations performed in this case.”); Ex. Q to Colson Aff., *Statistical Evaluation* at 380 (“Open source software is highly desirable in the court environment because openness to scrutiny by any interested party is an invaluable source of bug reports and suggestions for improvement.”) Many other statistical DNA programs are open source. *See* Ex. Q to Colson Aff., *Statistical Evaluation* at 376, Table 3 (Forensim, likeLTD, and DNAmixtures are open source). The FST is not.

Nor is the actual FST program available to the scientific community to test. Other statistical programs provide a link to their software so that other scientists may run the evidence in question through the program and test how different parameters may affect the results. *Cf.* Michael D. Coble and John M. Butler, *Exploring the Capabilities of Mixture Interpretation*

*Using True Allele Software*, National Institute of Standards and Technology presents the 24th Congress of the International Society for Forensic Genetics, Sept. 3, 2011, *available at* [http://www.cstl.nist.gov/strbase/pub\\_pres/ISFG2011-Coble-TrueAllele.pdf](http://www.cstl.nist.gov/strbase/pub_pres/ISFG2011-Coble-TrueAllele.pdf) (conducting study on TrueAllele software). The OCME does not permit this. This lack of transparency is atypical, and it prevents the relevant scientific community from assessing the FST's reliability.

Because OCME has failed to perform and/or disclose important studies, and experts have not been permitted to review the FST source code or test the software program, the FST fails the peer review requirement under *Daubert*.

#### **D.**

##### **FST is Not Generally Accepted in the Scientific Community**

The statistical evaluation of DNA mixture evidence is a relatively new field. The FST is just one of several competing software programs that have emerged in recent years. While each of these programs employs a different statistical model, the FST stands alone in how it determines drop-out rates. As discussed above, its methodology has been soundly rejected by other program developers and by the wider scientific community. Experts criticize OCME's failure to account for the unique characteristics of real crime-scene samples; the failure to test several primary assumptions, such as the possible dependence of drop-out across alleles; and the failure to further investigate ambiguous results. Experts further criticize OCME's claim that it takes a "conservative" approach to estimating the LR. On the contrary, these experts argue that underestimating the drop-out rate and assuming the minimum number of contributors creates a substantial danger of prejudicing the defense.

Significantly, after an extensive *Frye* hearing, a New York State court recently found that the FST is not generally accepted in the scientific community. The Court's finding is persuasive evidence that the FST does not meet the *Daubert* standards and should not be accepted here. *See*

*Daubert*, 509 U.S. at 594 (“a known technique which has been able to attract only minimal support within the community’ may be properly viewed with skepticism”) (quoting *United States v. Downing*, 753 F.2d 1224, 1238 (3d Cir. 1985)).

### **E.**

#### **The FST Is Unreliable and Prejudicial When Applied to the Specific Facts of this Case**

In addition to making a determination regarding the independent reliability of a scientific methodology, courts also must examine reliability “in light of the particular facts of the particular case.” *Kumho Tire Co., Ltd.*, 526 U.S. at 158. The sheer power associated with scientific evidence—especially DNA evidence—warrants the Court’s careful review of the testing performed in this case. *See Daubert*, 508 U.S. at 595 (“Expert evidence can be both powerful and quite misleading....Because of this risk, the judge in weighing possible prejudice ...exercises more control over experts than over lay witnesses.”) (citation omitted). OCME failed to apply its own protocols to the testing or interpretation of the evidence here, and its ultimate conclusions are confusing, misleading, and highly prejudicial to Mr. Smalls. OCME’s clear missteps compound the problems inherent in the FST software and provide an additional basis for exclusion of the evidence, both under *Daubert* and Federal Rule of Evidence 403.

#### **1. OCME’s Protocols for Testing the Evidence are Not Substantiated by the Validation Studies**

OCME’s findings as to the grip area in its June 4, 2014, report are inherently unreliable because the protocols used for testing the evidence were not substantiated by the validation studies.

First, OCME performed the FST under the assumption that the mixture contained the DNA of “at least three people,” but according to OCME’s own validation study, the mixture included at least four people’s DNA. The greatest number of alleles a single person can have

across 15 loci is 30. Chakraborty Decl. ¶ 49. Most individuals have fewer than 30 alleles because they are homozygous at certain locations. *Id.* Based on its validation study, the maximum number of alleles OCME expects to see in a three-person mixture is 64. *See* Ex. L to Colson Aff., *Contributor Estimate Study* at 320, Table 3. Where there are more than 67 alleles in a mixture, OCME considers it a four-person mixture. *See id.* at 321 (67 or more alleles signified a 4-person mixture.) The forensic sample from the grip area contained 69 distinct alleles. *See* Ex. E to Colson Aff. at SMALLS0228. Thus, according to OCME's own validation studies, it should have viewed the evidence as a four-person mixture. Had it done so, the LR undoubtedly would have differed, as the number of contributors is a key input to the FST. Chakraborty Decl. ¶ 49.

The problem is that OCME has never completed validation studies on four-person mixtures. Ex. K to Colson Aff., *FST Validation Study* at 750 (FST developed for mixtures of two and three contributors); *see id.* at 759 ("FST is currently online for analysis of two- or three-person mixtures. Validation of four-person models is currently in progress.") Thus, it has no method for calculating LRs on a four-person sample. Nor has the FST specifically been approved for use on four-person samples. Chakraborty Decl. ¶ 49. OCME's misapplication of the FST to a four-person mixture here, when the software has never been validated for that purpose, clearly renders its LR unreliable under *Daubert*. *Amorgianos*, 303 F.3d at 266 (holding that misapplication of a reliable methodology renders it unreliable).

Second, even assuming *arguendo* the DNA extracted from the grip area could reasonably be deemed a three-person mixture, OCME's validation studies still fail to address the specific facts of this case. The studies tested three-person mixtures, but they never tested three-person *degraded* mixtures. *See* Ex. K to Colson Aff., *FST Validation Study* at 752 (itemizing the mock

evidence samples used in the validation study, which included the specimens from two-person mixtures with DNA that was degraded in the laboratory, but not three-person mixtures). And the DNA extracted from the grip area was undoubtedly degraded. The electropherogram of the grip area sample, *see* Ex. C to Colson Aff. at SMALLS0159, shows a classic “ski slope” effect. Chakraborty Decl. ¶ 50. The “ski slope” effect is the decrease in size of the peak heights from left to right across the allelic positions. *Id.* In the grip area electropherogram, the peak heights are approximately 70% higher on the left than the right. *Id.* The “ski slope effect” is a well-accepted indicator of degradation in the scientific community. *Id.* It is clearly recognized by OCME. *See* Ex. K to Colson Aff., *FST Validation Study* at 759 (signs of degradation include the “ski slope effect.”) And, of course, degradation of the sample should come as no surprise considering that the gun was allegedly touched by multiple people, thrown to the ground, moved, and ultimately found sitting on top of a car tire.

Thus, even assuming the sample could reasonably be deemed a three-person mixture, OCME’s misapplication of the FST to a three-person *degraded* mixture also renders the LR unreliable under *Daubert*. *Amorgianos*, 303 F.3d at 266 (holding that misapplication of a reliable methodology renders it unreliable).

2. OCME Did Not Properly Apply its Own Protocols to the Testing and Interpretation of the Slide Grip Grooves, and its Inconclusive Finding is Misleading and Prejudicial

In its initial report, dated January 9, 2014, the OCME determined that all three swabs, including the one from the slide grip grooves, were suitable for comparison. *See* Ex. E to Colson at SMALLS0093. However, OCME only performed the FST on the swab from the grip area.

Mr. Smalls was excluded as a contributor to the sample from the trigger and trigger guard without performance of the FST. But he was not excluded as a contributor to the sample from the slide grip grooves. Instead, OCME compared the number of DNA alleles seen in the profile

of Mr. Smalls with those from the slide grip grooves mixture and found that “it cannot be determined whether they [Mr. Smalls’ alleles] can or cannot be excluded as a contributor to the mixture.” Ex. E to Colson Aff. at SMALLS0212.

OCME’s conclusion as to the slide grip grooves is confusing, especially to the lay person. Moreover, whatever its meaning, OCME arrived at this determination only by ignoring its own protocol for using the FST. Simply comparing alleles may allow for the *exclusion* of Mr. Smalls as a contributor. But nowhere in the FST protocol does it provide that comparing alleles may justify an *inconclusive* determination. To the contrary, the FST protocol directs that the software itself should be used whenever “[t]he DNA profiles of the major and the minor contributors cannot be determined; however, the sample is informative and suitable for comparison.” Ex. J to Colson Aff., OCME Forensic STR Analysis Protocol, at 440. The sample from the slide grip grooves was found suitable for comparison. Thus, according to its own protocol, OCME should have used the FST on that sample. Having failed to do so, there is no basis for stating it “cannot be determined” whether or not Mr. Smalls contributed. Chakraborty Decl. ¶ 51. Since comparing alleles on a sample suitable for FST testing is improper under OCME guidelines, OCME’s inconclusive finding as to the slide slip grooves has no scientific value and should be excluded under *Daubert*.<sup>13</sup>

The conclusion as to the slide grip grooves is also misleading and unduly prejudicial to Mr. Smalls. This is because it suggests he *may* have touched the slide grip grooves, when

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<sup>13</sup> In addition, that the OCME performed FST on the grip area, but not on the slide grip grooves (where the evidence against Mr. Smalls was clearly weaker), calls into question whether the OCME selectively applies the FST in favor of the prosecution. The possibility of bias is particularly strong here, as the OCME was on notice that Mr. Smalls was a “POI” or person of interest in Homicide before the FST was performed. Ex. E to Colson Aff. at SMALLS0226.

OCME has no actual evidence to support this implication. Thus, this evidence should also be excluded under Federal Rule of Evidence 403.

3. OCME's Conclusion that there is "Very Strong Support" that Mr. Smalls and Two Unknown Persons Contributed to the Grip Area is Misleading and Prejudicial

Under the FST protocol, a qualitative interpretation is given to express the strength of the hypothesis presented. In this case, OCME determined there is "very strong support" for the LR of 4,190 it calculated on the sample from the grip area. This interpretation is conclusive yet entirely subjective; OCME does not even attempt to provide a scientific basis for it. Chakraborty Decl ¶ 54. At the same time, it is also misleading. The precision of the number 4,190, by itself, implies scientific accuracy. The appearance of accuracy is then compounded by OCME's conclusion that the number provides "very strong support" for the prosecution hypothesis. Such simple and powerful language is likely to resonate with a jury, especially if other aspects of the expert testimony are difficult to understand. *See Williams*, 583 F.2d at 1199-2000 (Court should appraise potential for the jury to be awed the "mystic infallibility" surrounding scientific techniques.) Given the tremendous uncertainties as to the accuracy of the LRs generated by FST, the introduction of this qualitative interpretation will materially prejudice Mr. Smalls, providing another basis for exclusion under Federal Rule of Evidence 403.

4. The Quantitation Value Used to Determine the LR on the Grip Area May Be Inaccurate

As stated above, what distinguishes the FST's methodology from other statistical software programs is its use of DNA quantity to determine the LR. The reliability of the LR thus depends on the accurate measure of the quantity of DNA in a sample. According to OCME protocol, the lowest efficiency value in quantifying DNA in a sample is .80. *See Forensic Biology Protocols for Forensic STR Analysis*

<http://www.nyc.gov/html/ocme/downloads/pdf/Fbio/Protocols%20for%20Forensic%20STR%20Analysis.pdf> at 117. If the efficiency value of a quantification is lower than .80, it fails, and the sample must be quantified again. Here, the efficiency value was .80722, meaning it just barely passed OCME's own protocol. *See* Ex. C to Colson Aff. at SMALLS0117. The borderline efficiency of the sample, alone, calls into question the accuracy of the LR ratio here.

What is even more disturbing, however, is that in calculating the efficiency of the quantitation, OCME "clicked off" or ignored the standards from three of the fourteen control standard wells. The control standard wells are used to construct a "standard curve," which is the basis for the quantitation of all the samples. The efficiency value is a critical measurement of the accuracy of the standard curve. While "clicking off" certain standards is permissible, we do not know OCME's reasons for "clicking off" here. We requested those reasons on discovery and were told it was "unduly burdensome" for OCME to provide the data. One possibility, of course, is that OCME's inclusion of those wells in the overall efficiency calculation would have resulted in an efficiency value below .80. If this is true, then the sample would have failed OCME's efficiency protocol, and OCME should not have calculated a LR at all. Absent the data we requested, we can only raise the question. It is the government's burden to establish the reliability of its LR.

#### IV.

#### **CONCLUSION**

The statistical evaluation of DNA profile evidence is evolving, but it is still a relatively new field, and there is no standard methodology for evaluating DNA mixtures. At the moment, there are several competing software programs. OCME is the only laboratory in the world to use the FST, and the program has only been online for several years.

To our knowledge, no federal court has introduced FST evidence over a defense objection. Recently, a Supreme Court judge in Kings County excluded the introduction of FST evidence in the combined cases of *Peaks & Collins*.

The Court's ruling in *Peaks & Collins* was correct, and this Court should follow it here. The FST stands alone in its use of pre-set drop-out rates based on quantitation. This methodology has been soundly rejected by OCME's competitors and by the wider scientific community because it fails to account for the features of real-world crime scene samples and can have the effect of making the LR higher, prejudicing the defense. Moreover, the program itself has not been subjected to adequate peer review as the source code has not been published, and the software is not available for public use and inspection.

OCME's specific missteps in this case further compound the problems inherent in the FST software. OCME failed to properly apply its own protocols to the testing and interpretation of the evidence from the grip area or the slide grip grooves, and the results of its tests are confusing and prejudicial to Mr. Smalls. Moreover, OCME's qualitative interpretation of the evidence as providing "very strong support" for the prosecution hypothesis is conclusive, entirely subjective, and dangerously misleading.

The cumulative flaws in the FST, both independently and as applied to the facts of this case, render the government's DNA evidence unreliable and prejudicial to Mr. Smalls. The Court should grant an evidentiary hearing and exclude the evidence under *Daubert* and Federal Rules of Evidence 702 and 403.

Dated: New York, N.Y.  
January 22, 2015

/s/

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Deborah A. Colson  
Kristen M. Santillo